Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Claims 1-26 (Canceled).

27. (Previously presented) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

SEQ ID NO:68;

nucleotides 6905-6930 (SEQ ID NO:46), 7055-7077 (SEQ ID NO:48), 7360-7384 (SEQ ID NO:49), 7832-7857 (SEQ ID NO:52), 8844-8869 (SEQ ID NO:53), 7629-7647 (SEQ ID NO:55), and 8224-8242 (SEQ ID NO:56) of the *env* gene of HIV-1 Bru;

E3

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nucleotides 6930-6905 (SEQ ID NO:47), 7384-7360 (SEQ ID NO:50), 7857-7832 (SEQ ID NO:51), 8869-8844 (SEQ ID NO:54), and nucleotides 8242-8224 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928 (SEQ ID NO:46), 7053-7075 (SEQ ID NO:48), 7349-7373 (SEQ ID NO:49), 7821-7846 (SEQ ID NO:52), 7612-7630 (SEQ ID NO:55), 8213-8231 (SEQ ID NO:56), and 8836-8861 (SEQ ID NO:53) of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903 (SEQ ID NO:47), 7373-7349 (SEQ ID NO:50), 7846-7821 (SEQ ID NO:51), 8861-8836 (SEQ ID NO:54), and 8231-8213 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

nucleotides 6860-6885 (SEQ ID NO:46), 7010-7032 (SEQ ID NO:48), 7306-7330 (SEQ ID NO:49), 7775-7800 (SEQ ID NO:52), 8787-8812 (SEQ ID NO:53), 7572-7590 (SEQ ID NO:55), and 8167-8185 (SEQ ID NO:56) of the *env* gene of HIV-1 Eli; and

nucleotides 6885-6860 (SEQ ID NO:47), 7330-7306 (SEQ ID NO:50), 7800-7775 (SEQ ID NO:51), 8812-8787 (SEQ ID NO:54), and 8185-8167 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

28. (Previously presented) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

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a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);

MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);

MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);

MMy7: ATC CTC AGG AGG GGA CCC AGA AAT T (SEQ ID NO:49);

MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);

MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);

MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56); and

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57);

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

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d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

Claims 29-31 (Canceled).

32. (Previously presented) A composition comprising at least one polypeptide according to claim 27 in combination with a pharmaceutically acceptable vehicle.

33. (Previously presented) A composition comprising at least one polypeptide according to claim 28 in combination with a pharmaceutically acceptable vehicle.

Claims 34-37 (Canceled).

38. (Previously presented) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

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a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

SEQ ID NO:68;

nucleotides 6905-6930 (SEQ ID NO:46), 7055-7077 (SEQ ID NO:48), 7360-7384 (SEQ ID NO:49), 7832-7857 (SEQ ID NO:52), 8844-8869 (SEQ ID NO:53), 7629-7647 (SEQ ID NO:55), and 8224-8242 (SEQ ID NO:56) of the *env* gene of HIV-1 Bru;

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nucleotides 6930-6905 (SEQ ID NO:47), 7384-7360 (SEQ ID NO:50), 7857-7832 (SEQ ID NO:51), 8869-8844 (SEQ ID NO:54), and nucleotides 8242-8224 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Bru;

nucleotides 6903-6928 (SEQ ID NO:46), 7053-7075 (SEQ ID NO:48), 7349-7373 (SEQ ID NO:49), 7821-7846 (SEQ ID NO:52), 7612-7630 (SEQ ID NO:55), 8213-8231 (SEQ ID NO:56), and 8836-8861 (SEQ ID NO:53) of the *env* gene of HIV-1 Mal;

nucleotides 6928-6903 (SEQ ID NO:47), 7373-7349 (SEQ ID NO:50), 7846-7821 (SEQ ID NO:51), 8861-8836 (SEQ ID NO:54), and 8231-8213 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Mal;

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nucleotides 6860-6885 (SEQ ID NO:46), 7010-7032 (SEQ ID NO:48), 7306-7330 (SEQ ID NO:49), 7775-7800 (SEQ ID NO:52), 8787-8812 (SEQ ID NO:53), 7572-7590 (SEQ ID NO:55), and 8167-8185 (SEQ ID NO:56) of the *env* gene of HIV-1 Eli;

nucleotides 6885-6860 (SEQ ID NO:47), 7330-7306 (SEQ ID NO:50), 7800-7775 (SEQ ID NO:51), 8812-8787 (SEQ ID NO:54), and 8185-8167 (SEQ ID NO:57) of a nucleic acid sequence complementary to the *env* gene of HIV-1 Eli; and

a nucleotide sequence that is not identical to anyone of SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, or SEQ ID NO:68, but is nonetheless capable of hybridizing with a nucleotide sequence of the *env* gene of HIV-1 Bru, HIV-1 Mal, and HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

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d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

39. (Previously presented) A polypeptide fragment of a viral protein encoded by a nucleotide sequence from a viral genome selected from the group consisting of HIV-1, HIV-2, and SIV and expressed by a method comprising:

a) amplifying the nucleic acid encoding said polypeptide with at least two primers, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said genome, said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said genome, wherein said regions of nucleotides are separated by about 100 to about 1100 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid, and said primers are selected from the group of nucleotides oriented in the 5' to 3' direction consisting of:

E3 cont'd

MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC (SEQ ID NO:46);

MMy5a: GGG GCA CAA TAA TGT ATG GGA ATT GG (SEQ ID NO:47);

MMy6: AAT GGC AGT CTA GCA GAA GAA GA (SEQ ID NO:48);

MMy7: ATC CTC AGG AGG GGA CCC AGA AAT T (SEQ ID NO:49);

MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T (SEQ ID NO:50);

MMy8: GTG CTT CCT GCT GCT CCC AAG AAC CC (SEQ ID NO:51);

MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC (SEQ ID NO:52);

MMy9: ATG GGT GGC AAG TGG TCA AAA AGT AG (SEQ ID NO:53);

ATG GGT GGC AAA TGG TCA AAA AGT AG (SEQ ID NO:68);

MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT (SEQ ID NO:54);

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MMy78: TAT TAA CAA GAG ATG GTG G (SEQ ID NO:55);

MMy89: CCA GCA AGA AAA GAA TGA A (SEQ ID NO:56);

MMy89a: TTC ATT CTT TTC TTG CTG G (SEQ ID NO:57); and

a nucleotide sequence that is not identical to anyone of SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, or SEQ ID NO:68, but is nonetheless capable of hybridizing with a nucleotide sequence of the *env* gene of HIV-1 Bru, HIV-1 Mal, and HIV-1 Eli;

b) introducing said amplified nucleotide sequence into a vector;

c) transforming a host cell with said vector;

d) placing said transformed host cell in culture; and

e) recovering said polypeptide from said culture.

Claims 40-42 (Canceled).

43. (Previously presented) A composition comprising at least one polypeptide according to claim 38 in combination with a pharmaceutically acceptable vehicle.

44. (Previously presented) A composition comprising at least one polypeptide according to claim 39 in combination with a pharmaceutically acceptable vehicle.

Claims 45-48 (Canceled).

49. (New) The polypeptide according to claim 27, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

50. (New) The polypeptide according to claim 28, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

E3 cont'd

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51. (New) The polypeptide according to claim 38, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

52. (New) The polypeptide according to claim 39, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

53. (New) The polypeptide according to claim 49, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

54. (New) The polypeptide according to claim 50, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

55. (New) The polypeptide according to claim 51, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

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56. (New) The polypeptide according to claim 52, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

57. (New) The composition according to claim 32, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

58. (New) The composition according to claim 33, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

59. (New) The composition according to claim 43, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

60. (New) The composition according to claim 44, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, HIV-1 Eli, HIV-2 ROD, or SIV-1 MAC.

61. (New) The composition according to claim 57, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

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62. (New) The composition according to claim 58, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

E3 concld

63. (New) The composition according to claim 59, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

64. (New) The composition according to claim 60, wherein the viral genome is HIV-1 Bru, HIV-1 Mal, or HIV-1 Eli.

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